

CRF Errors Corrected by the STIC System Branch

0590
1011
0185
#7

Serial Number: 101072,830

CRF Processing Date: 10/23/02
Edited by: DC
Verified by: DC (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: **ENTERED**
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIPE

RAW SEQUENCE LISTING

DATE: 10/23/2002

PATENT APPLICATION: US/10/072,830

TIME: 13:34:23

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF4\10232002\J072830.raw

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3 <110> APPLICANT: CHEN, DONG FENG
4   HUANG, XIZHONG
5   CHEN, GUANG
6   MANJI, HUSSEINI K.
8 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING AXON
9   REGENERATION AND PREVENTING NEURONAL CELL DEGENERATION
11 <130> FILE REFERENCE: ERM-105.01
13 <140> CURRENT APPLICATION NUMBER: 10/072,830
14 <141> CURRENT FILING DATE: 2002-02-08
16 <150> PRIOR APPLICATION NUMBER: 60/267,832
17 <151> PRIOR FILING DATE: 2001-02-09
19 <150> PRIOR APPLICATION NUMBER: 60/272,617
20 <151> PRIOR FILING DATE: 2001-03-01
22 <150> PRIOR APPLICATION NUMBER: 60/289,990
23 <151> PRIOR FILING DATE: 2001-05-10
25 <160> NUMBER OF SEQ ID NOS: 8
27 <170> SOFTWARE: PatentIn Ver. 2.1
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 1050
31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (32)..(748)
38 <400> SEQUENCE: 1
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40                               Met Ala His Ala Gly Arg Thr
41                               1           5
43 ggg tac gat aac cgg gag ata gtg atg aag tac atc cat tat aag ctg      100
44 Gly Tyr Asp Asn Arg Glu Ile Val Met Lys Tyr Ile His Tyr Lys Leu
45      10           15           20
47 tcg cag agg ggc tac gag tgg gat gcg gga gat gtg ggc gcc gcg ccc      148
48 Ser Gln Arg Gly Tyr Glu Trp Asp Ala Gly Asp Val Gly Ala Ala Pro
49      25           30           35
51 ccg ggg gcc gcc ccc gcg ccg ggc atc ttc tcc tcg cag ccc ggg cac      196
52 Pro Gly Ala Ala Pro Ala Pro Gly Ile Phe Ser Ser Gln Pro Gly His
53 40           45           50           55
55 acg ccc cat aca gcc gca tcc cgg gac ccg gtc gcc agg acc tcg ccg      244
56 Thr Pro His Thr Ala Ala Ser Arg Asp Pro Val Ala Arg Thr Ser Pro
57      60           65           70
59 ctg cag acc ccg gct gcc ccc ggc gcc gcc gcg ggg cct gcg ctc agc      292
60 Leu Gln Thr Pro Ala Ala Pro Gly Ala Ala Ala Gly Pro Ala Leu Ser
61      75           80           85

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63 ccg gtg cca cct gtg gtc cac ctg acc ctc cgc cag gcc ggc gac gac 340
64 Pro Val Pro Pro Val Val His Leu Thr Leu Arg Gln Ala Gly Asp Asp
65          90          95          100
67 ttc tcc cgc cgc tac cgc cgc gac ttc gcc gag atg tcc agg cag ctg 388
68 Phe Ser Arg Arg Tyr Arg Arg Asp Phe Ala Glu Met Ser Arg Gln Leu
69      105      110      115
71 cac ctg acg ccc ttc acc gcg cgg gga cgc ttt gcc acg gtg gtg gag 436
72 His Leu Thr Pro Phe Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu
73 120      125      130      135
75 gag ctc ttc agg gac ggg gtg aac tgg ggg agg att gtg gcc ttc ttt 484
76 Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe
77      140      145      150
79 gag ttc ggt ggg gtc atg tgt gtg gag agc gtc aac cgg gag atg tcg 532
80 Glu Phe Gly Gly Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser
81      155      160      165
83 ccc ctg gtg gac aac atc gcc ctg tgg atg act gag tac ctg aac cgg 580
84 Pro Leu Val Asp Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg
85      170      175      180
87 cac ctg cac acc tgg atc cag gat aac gga ggc tgg gat gcc ttt gtg 628
88 His Leu His Thr Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val
89      185      190      195
91 gaa ctg tac ggc ccc agc atg cgg cct ctg ttt gat ttc tcc tgg ctg 676
92 Glu Leu Tyr Gly Pro Ser Met Arg Pro Leu Phe Asp Phe Ser Trp Leu
93 200      205      210      215
95 tct ctg aag act ctg ctc agt ttg gcc ctg gtg gga gct tgc atc acc 724
96 Ser Leu Lys Thr Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr
97      220      225      230
99 ctg ggt gcc tat ctg ggc cac aag tgaagtcaac atgcctgccc caaacaata 778
100 Leu Gly Ala Tyr Leu Gly His Lys
101      235
103 tgcaaaaggt tcaactaaagc agtagaaata atatgcattg tcagtgatgt tccatgaaac 838
105 aaagctgcag gctgtttaag aaaaaataac acacatatata acatcacaca cacagacaga 898
107 cacacacaca cacaacaatt aacagtccttc aggcataaacg tcgaatcagc tattttactgc 958
109 caaagggaaa tatcatttat tttttacatt attaagaaaa aaagatttat ttattttaaga 1018
111 cagtcccatc aaaactcctg tctttggaaa tc 1050
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115 <211> LENGTH: 239
116 <212> TYPE: PRT
117 <213> ORGANISM: Homo sapiens
119 <400> SEQUENCE: 2
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121 1          5          10          15
123 Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
124      20      25      30
126 Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
127      35      40      45
129 Phe Ser Ser Gln Pro Gly His Thr Pro His Thr Ala Ala Ser Arg Asp
130      50      55      60
132 Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala

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133 65              70              75              80
135 Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Thr
136              85              90              95
138 Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe
139              100              105              110
141 Ala Glu Met Ser Arg Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
142              115              120              125
144 Arg Phe Ala Thr Val Val Glu Leu Phe Arg Asp Gly Val Asn Trp
145              130              135              140
147 Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
148 145              150              155              160
150 Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
151              165              170              175
153 Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
154              180              185              190
156 Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
157              195              200              205
159 Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
160              210              215              220
162 Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Gly His Lys
163 225              230              235
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168 <211> LENGTH: 926
169 <212> TYPE: DNA
170 <213> ORGANISM: Homo sapiens
172 <220> FEATURE:
173 <221> NAME/KEY: CDS
174 <222> LOCATION: (135)..(833)
176 <400> SEQUENCE: 3
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179 aaccagagac gagactcagt gagtgagcag gtgttttgga caatggactg gttgagccca 120
181 tccctattat aaaa atg tct cag agc aac cgg gag ctg gtg gtt gac ttt 170
182              Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe
183              1              5              10
185 ctc tcc tac aag ctt tcc cag aaa gga tac agc tgg agt cag ttt agt 218
186 Leu Ser Tyr Lys Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser
187              15              20              25
189 gat gtg gaa gag aac agg act gag gcc cca gaa ggg act gaa tcg gag 266
190 Asp Val Glu Glu Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser Glu
191              30              35              40
193 atg gag acc ccc agt gcc atc aat ggc aac cca tcc tgg cac ctg gca 314
194 Met Glu Thr Pro Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala
195 45              50              55              60
197 gac agc ccc gcg gtg aat gga gcc act gcg cac agc agc agt ttg gat 362
198 Asp Ser Pro Ala Val Asn Gly Ala Thr Ala His Ser Ser Ser Leu Asp
199              65              70              75
201 gcc cgg gag gtg atc ccc atg gca gca gta aag caa gcg ctg agg gag 410
202 Ala Arg Glu Val Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu
203              80              85              90

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205 gca ggc gac gag ttt gaa ctg cgg tac cgg cgg gca ttc agt gac ctg 458
206 Ala Gly Asp Glu Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu
207          95          100          105
209 aca tcc cag ctc cac atc acc cca ggg aca gca tat cag agc ttt gaa 506
210 Thr Ser Gln Leu His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu
211    110          115          120
213 cag gta gtg aat gaa ctc ttc cgg gat ggg gta aac tgg ggt cgc att 554
214 Gln Val Val Asn Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile
215 125          130          135          140
217 gtg gcc ttt ttc tcc ttc ggc ggg gca ctg tgc gtg gaa agc gta gac 602
218 Val Ala Phe Phe Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp
219          145          150          155
221 aag gag atg cag gta ttg gtg agt cgg atc gca gct tgg atg gcc act 650
222 Lys Glu Met Gln Val Leu Val Ser Arg Ile Ala Ala Trp Met Ala Thr
223          160          165          170
225 tac ctg aat gac cac cta gag cct tgg atc cag gag aac ggc ggc tgg 698
226 Tyr Leu Asn Asp His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp
227          175          180          185
229 gat act ttt gtg gaa ctc tat ggg aac aat gca gca gcc gag agc cga 746
230 Asp Thr Phe Val Glu Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser Arg
231    190          195          200
233 aag ggc cag gaa cgc ttc aac cgc tgg ttc ctg acg ggc atg act gtg 794
234 Lys Gly Gln Glu Arg Phe Asn Arg Trp Phe Leu Thr Gly Met Thr Val
235 205          210          215          220
237 gcc ggc gtg gtt ctg ctg ggc tca ctc ttc agt cgg aaa tgaccagaca 843
238 Ala Gly Val Val Leu Leu Gly Ser Leu Phe Ser Arg Lys
239          225          230
241 ctgaccatcc actctaccct cccacccctc tctctgtctc accacatcct ccgtccagcc 903
243 gccattgccca ccaggagaac cgg 926
246 <210> SEQ ID NO: 4
247 <211> LENGTH: 233
248 <212> TYPE: PRT
249 <213> ORGANISM: Homo sapiens
251 <400> SEQUENCE: 4
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253    1          5          10          15
255 Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser Asp Val Glu Glu
256          20          25          30
258 Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser Glu Met Glu Thr Pro
259          35          40          45
261 Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala Asp Ser Pro Ala
262          50          55          60
264 Val Asn Gly Ala Thr Ala His Ser Ser Ser Leu Asp Ala Arg Glu Val
265 65          70          75          80
267 Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu Ala Gly Asp Glu
268          85          90          95
270 Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu Thr Ser Gln Leu
271          100          105          110
273 His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu Gln Val Val Asn

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274      115      120      125
276 Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe
277      130      135      140
279 Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp Lys Glu Met Gln
280 145      150      155      160
282 Val Leu Val Ser Arg Ile Ala Ala Trp Met Ala Thr Tyr Leu Asn Asp
283      165      170      175
285 His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp Asp Thr Phe Val
286      180      185      190
288 Glu Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser Arg Lys Gly Gln Glu
289      195      200      205
291 Arg Phe Asn Arg Trp Phe Leu Thr Gly Met Thr Val Ala Gly Val Val
292      210      215      220
294 Leu Leu Gly Ser Leu Phe Ser Arg Lys
295 225      230
299 <210> SEQ ID NO: 5
300 <211> LENGTH: 20
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
304 <220> FEATURE:
305 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
307 <400> SEQUENCE: 5
308 gctgcagaca gactggccag                                20
311 <210> SEQ ID NO: 6
312 <211> LENGTH: 20
313 <212> TYPE: DNA
314 <213> ORGANISM: Artificial Sequence
316 <220> FEATURE:
317 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
319 <400> SEQUENCE: 6
320 aggcacgcgc cacatccagc                                20
323 <210> SEQ ID NO: 7
324 <211> LENGTH: 19
325 <212> TYPE: DNA
326 <213> ORGANISM: Artificial Sequence
328 <220> FEATURE:
329 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
331 <400> SEQUENCE: 7
332 ctggaagccg gcgcagatc                                19
335 <210> SEQ ID NO: 8
336 <211> LENGTH: 20
337 <212> TYPE: DNA
338 <213> ORGANISM: Artificial Sequence
340 <220> FEATURE:
341 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
343 <400> SEQUENCE: 8
344 gcgtgtccag gaagccttcc                                20

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/072,830

DATE: 10/23/2002

TIME: 13:34:24

Input Set : A:\PTO.DC.txt

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